



OIEP

RAW SEQUENCE LISTING

DATE: 04/17/2002

PATENT APPLICATION: US/10/054,435

TIME: 11:43:33

Input Set : N:\Cr3\RULE60\10054435.raw

Output Set: N:\CRF3\04172002\J054435.raw

1 <110> APPLICANT: Bollag, Gideon
 2 Crompton, Anne
 3 North, Anne
 4 Sharma, Sanju
 5 Roscoe, William
 6 <120> TITLE OF INVENTION: Methods and Compositions for Treating Abnormal Cell
 7 Growth Related to Unwanted Guanine Nucleotide Exchange
 8 Factor Activity
 9 <130> FILE REFERENCE: 1028-US
 10 <140> CURRENT APPLICATION NUMBER: 10/054,435
 11 <141> CURRENT FILING DATE: 2002-01-18
 13 <150> PRIOR APPLICATION NUMBER: 09/079,812
 14 <151> PRIOR FILING DATE: 1998-05-15
 16 <150> PRIOR APPLICATION NUMBER: 60/049,879
 17 <151> PRIOR FILING DATE: 1997-06-17
 18 <160> NUMBER OF SEQ ID NOS: 33
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 3171
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Liver Rac GEF
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 W--> 27 <222> LOCATION: Complement (76)..(2208)
 28 <400> SEQUENCE: 1
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 30 tctggctcta tttcc atg gag acc agg gaa tct gaa gat ttg gaa aag acc 111
 W--> 31 Met Glu Thr Arg Glu Ser Glu Asp Leu Glu Lys Thr
 32 1 5 10
 33 cgg agg aaa tca gca agt gat caa tgg aac act gat aat gaa cca gcc 159
 34 Arg Arg Lys Ser Ala Ser Asp Gln Trp Asn Thr Asp Asn Glu Pro Ala
 35 15 20 25
 36 aag gtg aaa cct gag tta ctc cca gaa aaa gag gag act tct caa gct 207
 37 Lys Val Lys Pro Glu Leu Leu Pro Glu Lys Glu Glu Thr Ser Gln Ala
 38 30 35 40
 39 gac cag gat atc caa gac aaa gag cct cat tgc cac atc cca att aag 255
 40 Asp Gln Asp Ile Gln Asp Lys Glu Pro His Cys His Ile Pro Ile Lys
 41 45 50 55 60
 42 aga aat tcc atc ttc aat cgc tcc ata aga cgc aaa agc aaa gcc aag 303
 43 Arg Asn Ser Ile Phe Asn Arg Ser Ile Arg Arg Lys Ser Lys Ala Lys
 44 65 70 75
 45 gcc aga gac aac ccc gaa cgg aac gcc agc tgc ctg gca gat tca cag 351
 46 Ala Arg Asp Asn Pro Glu Arg Asn Ala Ser Cys Leu Ala Asp Ser Gln

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47		80		85		90		
48	gac aat gga aaa tct gta aat gag ccc ctg acc ttg aat atc ccc tgg							399
49	Asp Asn Gly Lys Ser Val Asn Glu Pro Leu Thr Leu Asn Ile Pro Trp							
50		95		100		105		
51	agc aga atg cct cct tgc aga aca gca atg cag aca gac cca gga gcc							447
52	Ser Arg Met Pro Pro Cys Arg Thr Ala Met Gln Thr Asp Pro Gly Ala							
53		110		115		120		
54	cag gaa atg agt gag tgc tcc tcc acc ccg gga aat ggg gcc acg ccc							495
55	Gln Glu Met Ser Glu Ser Ser Ser Thr Pro Gly Asn Gly Ala Thr Pro							
56		125		130		135		140
57	gag gag tgg ccg gcc ctg gcc gac agc ccc acc acg ctc acc gag gcc							543
58	Glu Glu Trp Pro Ala Leu Ala Asp Ser Pro Thr Thr Leu Thr Glu Ala							
59		145		150		155		
60	ctg cgg atg atc cac ccc att ccc gcc gac tcc tgg aga aac ctc att							591
61	Leu Arg Met Ile His Pro Ile Pro Ala Asp Ser Trp Arg Asn Leu Ile							
62		160		165		170		
63	gaa caa ata ggg ctc ctg tat cag gaa tac cga gat aaa tcg act ctc							639
64	Glu Gln Ile Gly Leu Leu Tyr Gln Glu Tyr Arg Asp Lys Ser Thr Leu							
65		175		180		185		
66	caa gaa atc gaa acc agg agg caa cag gat gca gaa ata gaa gac aat							687
67	Gln Glu Ile Glu Thr Arg Arg Gln Gln Asp Ala Glu Ile Glu Asp Asn							
68		190		195		200		
69	acc aat ggg tcc ccg gcc agt gag gac acc ccg gag gag gaa gaa gaa							735
70	Thr Asn Gly Ser Pro Ala Ser Glu Asp Thr Pro Glu Glu Glu Glu Glu							
71		205		210		215		220
72	gag gag gag gag gag gag ccg gcc agc cca cca gag agg aag act ctg							783
73	Glu Glu Glu Glu Glu Glu Pro Ala Ser Pro Pro Glu Arg Lys Thr Leu							
74		225		230		235		
75	ccc cag atc tgc ctg ctc agt aac ccc cac tca agg ttc aac ctc tgg							831
76	Pro Gln Ile Cys Leu Leu Ser Asn Pro His Ser Arg Phe Asn Leu Trp							
77		240		245		250		
78	cag gat ctt ccc gag atc ccg agc agc ggg gtg ctt gag atc cta cag							879
79	Gln Asp Leu Pro Glu Ile Arg Ser Ser Gly Val Leu Glu Ile Leu Gln							
80		255		260		265		
81	cct gag gag att aag ctg cag gag gcc atg ttc gag ctg gtc act tcc							927
82	Pro Glu Glu Ile Lys Leu Gln Glu Ala Met Phe Glu Leu Val Thr Ser							
83		270		275		280		
84	gag gcg tcc tac tac aag agt ctg aac ctg ctc gtg tcc cac ttc atg							975
85	Glu Ala Ser Tyr Tyr Lys Ser Leu Asn Leu Leu Val Ser His Phe Met							
86		285		290		295		300
87	gag aac gag ccg ata agg aag atc ctg cac ccg tcc gag gcg cac atc							1023
88	Glu Asn Glu Arg Ile Arg Lys Ile Leu His Pro Ser Glu Ala His Ile							
89		305		310		315		
90	ctc ttc tcc aac gtc ctg gac gtg ctg gct gtc agt gag ccg ttc ctc							1071
91	Leu Phe Ser Asn Val Leu Asp Val Leu Ala Val Ser Glu Arg Phe Leu							
92		320		325		330		
93	ctg gag ctg gag cac ccg atg gag gag aac atc gtc atc tct gac gtg							1119
94	Leu Glu Leu Glu His Arg Met Glu Glu Asn Ile Val Ile Ser Asp Val							
95		335		340		345		

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96   tgt gac atc gtg tac cgt tat gcg gcc gac cac ttc tct gtc tac atc   1167
97   Cys Asp Ile Val Tyr Arg Tyr Ala Ala Asp His Phe Ser Val Tyr Ile
98       350                               355                               360
99   acc tac gtc agc aat cag acc tac cag gag cgg acc tat aag cag ctg   1215
100   Thr Tyr Val Ser Asn Gln Thr Tyr Gln Glu Arg Thr Tyr Lys Gln Leu
101   365                               370                               375                               380
102   ctc cag gag aag gca gct ttc cgg gag ctg atc gcg cag cta gag ctc   1263
103   Leu Gln Glu Lys Ala Ala Phe Arg Glu Leu Ile Ala Gln Leu Glu Leu
104       385                               390                               395
105   gac ccc aag tgc agg ggg ctg ccc ttc tcc ttc ctc atc ctg cct   1311
106   Asp Pro Lys Cys Arg Gly Leu Pro Phe Ser Ser Phe Leu Ile Leu Pro
107       400                               405                               410
108   ttc cag agg atc aca cgc ctc aag ctg ttg gtc cag aac atc ctg aag   1359
109   Phe Gln Arg Ile Thr Arg Leu Lys Leu Leu Val Gln Asn Ile Leu Lys
110       415                               420                               425
111   agg gta gaa gag agg tct gag cgg gag tgc act gct ttg gat gct cac   1407
112   Arg Val Glu Glu Arg Ser Glu Arg Glu Cys Thr Ala Leu Asp Ala His
113       430                               435                               440
114   aag gag ctg gaa atg gtg gtg aag gca tgc aac gag ggc gtc agg aaa   1455
115   Lys Glu Leu Glu Met Val Val Lys Ala Cys Asn Glu Gly Val Arg Lys
116   445                               450                               455                               460
117   atg agc cgc acg gaa cag atg atc agc att cag aag aag atg gag ttc   1503
118   Met Ser Arg Thr Glu Gln Met Ile Ser Ile Gln Lys Lys Met Glu Phe
119       465                               470                               475
120   aag atc aag tcg gtg ccc atc atc tcc cac tcc cgc tgg ctg ctg aag   1551
121   Lys Ile Lys Ser Val Pro Ile Ile Ser His Ser Arg Trp Leu Leu Lys
122       480                               485                               490
123   cag ggt gag ctg cag cag atg tca ggc ccc aag acc tcc cgg acc ctg   1599
124   Gln Gly Glu Leu Gln Gln Met Ser Gly Pro Lys Thr Ser Arg Thr Leu
125       495                               500                               505
126   agg acc aag aag ctc ttc cac gaa att tac ctc ttc ctg ttc aac gac   1647
127   Arg Thr Lys Lys Leu Phe His Glu Ile Tyr Leu Phe Leu Phe Asn Asp
128       510                               515                               520
129   ctg ctg gtg atc tgc cgg cag att cca gga gac aag tac cag gta ttt   1695
130   Leu Leu Val Ile Cys Arg Gln Ile Pro Gly Asp Lys Tyr Gln Val Phe
131   525                               530                               535                               540
132   gac tca gct ccg cgg gga ctg ctg cgt gtg gag gag ctg gag gac cag   1743
133   Asp Ser Ala Pro Arg Gly Leu Leu Arg Val Glu Glu Leu Glu Asp Gln
134       545                               550                               555
135   ggc cag acg ctg gcc aac gtg ttc atc ctg cgg ctg ctg gag aac gca   1791
136   Gly Gln Thr Leu Ala Asn Val Phe Ile Leu Arg Leu Leu Glu Asn Ala
137       560                               565                               570
138   gat gac cgg gag gcc acc tac atg cta aag gcg tcc tct cag agt gag   1839
139   Asp Asp Arg Glu Ala Thr Tyr Met Leu Lys Ala Ser Ser Gln Ser Glu
140       575                               580                               585
141   atg aag cgt tgg atg acc tca ctg gcc ccc aac agg agg acc aag ttt   1887
142   Met Lys Arg Trp Met Thr Ser Leu Ala Pro Asn Arg Arg Thr Lys Phe
143       590                               595                               600
144   gtt tcg ttc aca tcc cgg ctg ctg gac tgc ccc cag gtc cag tgc gtg   1935

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145 Val Ser Phe Thr Ser Arg Leu Leu Asp Cys Pro Gln Val Gln Cys Val
146 605 610 615 620
147 cac cca tac gtg gct cag cag cca gac gag ctg acg ctg gag ctc gcc 1983
148 His Pro Tyr Val Ala Gln Gln Pro Asp Glu Leu Thr Leu Glu Leu Ala
149 625 630 635
150 gag atc ctc aac atc ctg gac aag act gag gac ggg tgg atc ttt ggc 2031
151 Asp Ile Leu Asn Ile Leu Asp Lys Thr Asp Asp Gly Trp Ile Phe Gly
152 640 645 650
153 gag cgt ctg cac gac cag gag aga ggc tgg ttc ccc agc tcc atg act 2079
154 Glu Arg Leu His Asp Gln Glu Arg Gly Trp Phe Pro Ser Ser Met Thr
155 655 660 665
156 gag gag atc ttg aat ccc aag atc cgg tcc cag aac ctc aag gaa tgt 2127
157 Glu Glu Ile Leu Asn Pro Lys Ile Arg Ser Gln Asn Leu Lys Glu Cys
158 670 675 680
159 ttc cgt gtc cac aag atg gat gac cct cag cgc agc cag aac aag gac 2175
160 Phe Arg Val His Lys Met Asp Asp Pro Gln Arg Ser Gln Asn Lys Asp
161 685 690 695 700
162 cgc agg aag ctg ggc agc cgg aat cgg caa tga ccccccaccca gggggccagc 2228
163 Arg Arg Lys Leu Gly Ser Arg Asn Arg Gln
164 705 710
165 gggagcaggg cctgcatgag accccgacag aaggtggggg gggggggggg ggctctggga 2288
166 agcacaggcc agcacctccc caggtggcag gatctggctt ggggtgcccg gccctcatcc 2348
167 ctgcccacgc agtgagtgtc catgtgtctt ggccccttgc tcgcaaactg gataaagggg 2408
168 gcccaagcct ctctgatgc atttgtaaac aagaaggttt cagcagtatt acaccacctc 2468
169 cctcatgcct ccgagggggg ggaagggggg gggcacactc caggggcccc catgcccctg 2528
170 gccccaggg attggaagag gctcccaacc cagagtgtcc ctgtgggagg caggcagaag 2588
171 gtgacaattg acacgatttc ctgcacgcgt cttcttttac cttggaagca gttagaattt 2648
172 accaggcaca gatgaggccg cccttgccctg acggagcttg atgagcagcc cttggtctcc 2708
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176 cccaggtgtt ttaaggaatg aattggtcac tgcacttgtt atcgattatg gttctgagaa 2948
177 aagcaaatat cggaattcct gcagcccggg aaatggggcc acgcccaggg agtggccggc 3008
178 cctggccgac agccccacca cgctcaccga ggccctgcgg atgatccacc ccattcccgc 3068
179 cgactcctgg agaaacctca ttgaacaaat agggctcctg tatcaggaat accgagataa 3128
180 atcgactctc caaaaaaaaa aaaaaaaaaa gatctttaat taa 3171
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 710
184 <212> TYPE: PRT
185 <213> ORGANISM: Liver Rac GEF
186 <400> SEQUENCE: 2
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188 1 5 10 15
189 Ala Ser Asp Gln Trp Asn Thr Asp Asn Glu Pro Ala Lys Val Lys Pro
190 20 25 30
191 Glu Leu Leu Pro Glu Lys Glu Glu Thr Ser Gln Ala Asp Gln Asp Ile
192 35 40 45
193 Gln Asp Lys Glu Pro His Cys His Ile Pro Ile Lys Arg Asn Ser Ile
194 50 55 60

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195   Phe Asn Arg Ser Ile Arg Arg Lys Ser Lys Ala Lys Ala Arg Asp Asn
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198                      85                      90                      95
199   Ser Val Asn Glu Pro Leu Thr Leu Asn Ile Pro Trp Ser Arg Met Pro
200                      100                     105                     110
201   Pro Cys Arg Thr Ala Met Gln Thr Asp Pro Gly Ala Gln Glu Met Ser
202                      115                     120                     125
203   Glu Ser Ser Ser Thr Pro Gly Asn Gly Ala Thr Pro Glu Glu Trp Pro
204                      130                     135                     140
205   Ala Leu Ala Asp Ser Pro Thr Thr Leu Thr Glu Ala Leu Arg Met Ile
206                      145                     150                     155                     160
207   His Pro Ile Pro Ala Asp Ser Trp Arg Asn Leu Ile Glu Gln Ile Gly
208                      165                     170                     175
209   Leu Leu Tyr Gln Glu Tyr Arg Asp Lys Ser Thr Leu Gln Glu Ile Glu
210                      180                     185                     190
211   Thr Arg Arg Gln Gln Asp Ala Glu Ile Glu Asp Asn Thr Asn Gly Ser
212                      195                     200                     205
213   Pro Ala Ser Glu Asp Thr Pro Glu Glu Glu Glu Glu Glu Glu Glu
214                      210                     215                     220
215   Glu Glu Pro Ala Ser Pro Pro Glu Arg Lys Thr Leu Pro Gln Ile Cys
216                      225                     230                     235                     240
217   Leu Leu Ser Asn Pro His Ser Arg Phe Asn Leu Trp Gln Asp Leu Pro
218                      245                     250                     255
219   Glu Ile Arg Ser Ser Gly Val Leu Glu Ile Leu Gln Pro Glu Glu Ile
220                      260                     265                     270
221   Lys Leu Gln Glu Ala Met Phe Glu Leu Val Thr Ser Glu Ala Ser Tyr
222                      275                     280                     285
223   Tyr Lys Ser Leu Asn Leu Leu Val Ser His Phe Met Glu Asn Glu Arg
224                      290                     295                     300
225   Ile Arg Lys Ile Leu His Pro Ser Glu Ala His Ile Leu Phe Ser Asn
226                      305                     310                     315                     320
227   Val Leu Asp Val Leu Ala Val Ser Glu Arg Phe Leu Leu Glu Leu Glu
228                      325                     330                     335
229   His Arg Met Glu Glu Asn Ile Val Ile Ser Asp Val Cys Asp Ile Val
230                      340                     345                     350
231   Tyr Arg Tyr Ala Ala Asp His Phe Ser Val Tyr Ile Thr Tyr Val Ser
232                      355                     360                     365
233   Asn Gln Thr Tyr Gln Glu Arg Thr Tyr Lys Gln Leu Leu Gln Glu Lys
234                      370                     375                     380
235   Ala Ala Phe Arg Glu Leu Ile Ala Gln Leu Glu Leu Asp Pro Lys Cys
236                      385                     390                     395                     400
237   Arg Gly Leu Pro Phe Ser Ser Phe Leu Ile Leu Pro Phe Gln Arg Ile
238                      405                     410                     415
239   Thr Arg Leu Lys Leu Leu Val Gln Asn Ile Leu Lys Arg Val Glu Glu
240                      420                     425                     430
241   Arg Ser Glu Arg Glu Cys Thr Ala Leu Asp Ala His Lys Glu Leu Glu
242                      435                     440                     445
243   Met Val Val Lys Ala Cys Asn Glu Gly Val Arg Lys Met Ser Arg Thr

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L:31 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 1, CDS LOCATION:0..76

L:474 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:30, CDS LOCATION: Complement (1)..(198)